

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Soo Y.
Choi, Yongwon
- (ii) TITLE OF INVENTION: SIGNAL TRANSDUCER FOR THE TNF RECEPTOR SUPER FAMILY, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/052,089
(B) FILING DATE: 31-MAR-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 600-1-198 CIP 1
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Pro Ile Arg Ala Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His

1

5

10

15

Ser Arg Asp Val Ala Ala Ile His Cys Gly His Thr Phe His Leu Gln
20 25 30

Cys Leu Ile Gln Ser Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln
35 40 45

Cys Arg Ile Gln Val Gly Lys Arg Thr Ile Ile Asn Lys Leu Phe Phe
50 55 60

Asp Leu Ala Gln Glu Glu Glu Asn Val Leu Asp Arg Glu Phe Leu Lys
65 70 75 80

Asn Glu Leu Asp Asn Val Arg Ala Gln Leu Ser Gln Lys Asp Lys Glu
85 90 95

Lys Arg Asp Ser Gln Val Ile Ile Asp Thr Leu Arg Asp Thr Leu Glu
100 105 110

Glu Arg Asn Ala Thr Val Val Ser Leu Gln Gln Ala Leu Gly Lys Ala
115 120 125

Glu Met Leu Cys Ser Thr Leu Lys Lys Gln Met Lys Tyr Leu Glu Gln
130 135 140

Gln Gln Asp Glu Thr Lys Gln Ala Gln Glu Glu Ala Gly Arg Leu Arg
145 150 155 160

Ser Lys Met Lys Thr Met Glu Gln Ile Glu Leu Leu Leu Gln Ser Gln
165 170 175

Leu Pro Glu Val Glu Glu Met Ile Arg Asp Met Gly Val Gly Gln Ser
180 185 190

Ala Val Glu Gln Leu Ala Val Tyr Cys Val Ser Leu Lys Lys Glu Tyr
195 200 205

Glu Asn Leu Lys Glu Ala Arg Lys Ala Ser Gly Glu Val Ala Asp Lys
210 215 220

Leu Arg Lys Asp Leu Phe Ser Ser Arg Ser Lys Leu Gln Thr Val Tyr
225 230 235 240

Ser Glu Leu Asp Gln Ala Lys Leu Glu Leu Lys Ser Ala Gln Lys Asp
245 250 255

Leu Gln Ser Ala Asp Lys Glu Ile Met Ser Leu Lys Lys Leu Thr
260 265 270

Met Leu Gln Glu Thr Leu Asn Leu Pro Pro Val Ala Ser Glu Thr Val
275 280 285

Asp Arg Leu Val Leu Glu Ser Pro Ala Pro Val Glu Val Asn Leu Lys
290 295 300

Leu Arg Arg Pro Ser Phe Arg Asp Asp Ile Asp Leu Asn Ala Thr Phe
305 310 315 320

Asp Val Asp Thr Pro Pro Ala Arg Pro Ser Ser Ser Gln His Gly Tyr
325 330 335

Tyr Glu Lys Leu Cys Leu Glu Lys Ser His Ser Pro Ile Gln Asp Val
340 345 350

Cont
B1

*Cat
Pj*

Pro Lys Lys Ile Cys Lys Gly Pro Arg Lys Glu Ser Gln Leu Ser Leu
355 360 365
Gly Gly Gln Ser Cys Ala Gly Glu Pro Asp Glu Glu Leu Val Gly Ala
370 375 380
Phe Pro Ile Phe Val Arg Asn Ala Ile Leu Gly Gln Lys Gln Pro Lys
385 390 395 400
Arg Pro Arg Ser Glu Ser Ser Cys Ser Lys Asp Val Val Arg Thr Gly
405 410 415
Phe Asp Gly Leu Gly Gly Arg Thr Lys Phe Ile Gln Pro Thr Asp Thr
420 425 430
Val Met Ile Arg Pro Leu Pro Val Lys Pro Lys Thr Lys Val Lys Gln
435 440 445
Arg Val Arg Val Lys Thr Val Pro Ser Leu Phe Gln Ala Lys Leu Asp
450 455 460
Thr Phe Leu Trp Ser
465

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Ile Leu Ser Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His
1 5 10 15

Ser Arg Asp Val Ala Ala Ile His Cys Gly His Thr Phe His Leu Gln
20 25 30

Cys Leu Ile Gln Trp Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln
35 40 45

Cys Arg Ile Gln Val Gly Lys Lys Thr Ile Ile Asn Lys Leu Phe Phe
50 55 60

Asp Ile Ala Gln Glu Glu Glu Asn Val Leu Asp Ala Glu Phe Leu Lys
65 70 75 80

Asn Glu Leu Asp Ser Val Lys Ala Gln Leu Ser Gln Lys Asp Arg Glu
85 90 95

Lys Arg Asp Ser Gln Ala Ile Ile Asp Thr Leu Arg Asp Thr Leu Glu
100 105 110

Glu Arg Asn Ala Thr Val Glu Ser Leu Gln Asn Ala Leu Asn Lys Ala
115 120 125

Glu Met Leu Cys Ser Thr Leu Lys Lys Gln Met Lys Phe Leu Glu Gln
130 135 140

Arg Gln Asp Glu Thr Lys Gln Ala Arg Glu Ala His Arg Leu Lys
145 150 155 160

Cys Lys Met Lys Thr Met Glu Gln Ile Glu Leu Leu Leu Gln Ser Gln
165 170 175

Arg Ser Glu Val Glu Glu Met Ile Arg Asp Met Gly Val Gly Gln Ser
180 185 190

Ala Val Glu Gln Leu Ala Val Tyr Cys Val Ser Leu Lys Lys Glu Tyr
195 200 205

Glu Asn Leu Lys Glu Ala Arg Lys Ala Thr Gly Glu Leu Ala Asp Arg
210 215 220

Leu Lys Lys Asp Leu Val Ser Ser Arg Ser Lys Leu Lys Thr Leu Asn
225 230 235 240

Thr Glu Leu Asp Gln Ala Lys Leu Glu Leu Arg Ser Ala Gln Lys Asp
245 250 255

Leu Gln Ser Ala Asp Gln Glu Ile Thr Ser Leu Arg Lys Lys Ser Asp
260 265 270

Asp Pro Pro Gly Asn Leu Glu Pro Ala Ser Ala Thr Asn Glu Thr Val
275 280 285

Ser Arg Leu Val Phe Glu Ser Pro Ala Pro Val Glu Met Met Asn Pro
290 295 300

Arg Leu His Gln Pro Pro Phe Gly Asp Glu Ile Asp Leu Asn Thr Thr
305 310 315 320

Phe Asp Val Asn Thr Pro Pro Thr Gln Thr Ser Gly Ser Gln His Cys
325 330 335

Leu Pro Lys Lys Leu Cys Leu Glu Arg Ala Arg Ser Pro Met Gln Asn
340 345 350

Val Leu Lys Lys Val His Lys Val Ser Lys Pro Glu Ser Gln Leu Ser
355 360 365

Leu Gly Gly Gln Arg Cys Val Gly Glu Leu Asp Glu Glu Leu Ala Gly
370 375 380

Ala Phe Pro Leu Phe Ile Arg Asn Ala Val Leu Gly Gln Lys Gln Pro
385 390 395 400

Asn Arg Thr Thr Ala Glu Ser Arg Ser Ser Thr Asp Val Val Arg Ile
405 410 415

Gly Phe Asp Gly Leu Gly Gly Arg Thr Lys Phe Ile Gln Pro Arg Asp
420 425 430

Thr Thr Ile Ile Arg Pro Val Pro Val Lys Ser Lys Ala Lys Ser Lys
435 440 445

Gln Lys Val Arg Ile Lys Thr Val Ser Ser Ala Ser Gln Pro Lys Leu
450 455 460

Asp Thr Phe Leu Cys Gln
465 470

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Thr Ile Ile Asn Lys Leu Phe Phe Asp Leu Ala Gln Glu Glu Glu
1 5 10 15

Asn Val Leu Asp Arg Glu Phe Leu Lys Asn Glu Leu Asp Asn Val Arg
20 25 30

Ala Gln Leu Ser Gln Lys Asp Lys Glu Lys Arg Asp Ser Gln Val Ile
35 40 45

Ile Asp Thr Leu Arg Asp Thr Leu Glu Glu Arg Asn Ala Thr Val Val
50 55 60

Ser Leu Gln Gln Ala Leu Gly Lys Ala Glu Met Leu Cys Ser Thr Leu
65 70 75 80

Lys Lys Gln Met Lys Tyr Leu Glu Gln Gln Asp Glu Thr Lys Gln
85 90 95

Ala Gln Glu Glu Ala Gly Arg Leu Arg Ser Lys Met Lys Thr Met Glu
100 105 110

Gln Ile Glu Leu Leu Leu Gln Ser Gln Leu Pro Glu Val Glu Glu Met
115 120 125

Ile Arg Asp Met Gly Val Gly Gln Ser Ala Val Glu Gln Leu Ala Val
130 135 140

Tyr Cys Val Ser Leu Lys Lys Glu Tyr Glu Asn Leu Lys Glu Ala Arg
145 150 155 160

Lys Ala Ser Gly Glu Val Ala Asp Lys Leu Arg Lys Asp Leu Phe Ser
165 170 175

Ser Arg Ser Lys Leu Gln Thr Val Tyr Ser Glu Leu Asp Gln Ala Lys
180 185 190

Leu Glu Leu Lys Ser Ala Gln Lys Asp Leu Gln Ser Ala Asp Lys Glu
195 200 205

Ile Met Ser Leu Lys Lys Leu Thr Met Leu Gln
210 215 220

(2) INFORMATION FOR SEQ ID NO:4:

- Contd*
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Thr Ile Ile Asn Lys Leu Phe Phe Asp Ile Ala Gln Glu Glu Glu
1 5 10 15

Asn Val Leu Asp Ala Glu Phe Leu Lys Asn Glu Leu Asp Ser Val Lys
20 25 30

Ala Gln Leu Ser Gln Lys Asp Arg Glu Lys Arg Asp Ser Gln Ala Ile
35 40 45

Ile Asp Thr Leu Arg Asp Thr Leu Glu Glu Arg Asn Ala Thr Val Glu
50 55 60

Ser Leu Gln Asn Ala Leu Asn Lys Ala Glu Met Leu Cys Ser Thr Leu
65 70 75 80

Lys Lys Gln Met Lys Phe Leu Glu Gln Arg Gln Asp Glu Thr Lys Gln
85 90 95

Ala Arg Glu Glu Ala His Arg Leu Lys Cys Lys Met Lys Thr Met Glu
100 105 110

Gln Ile Glu Leu Leu Gln Ser Gln Arg Ser Glu Val Glu Glu Met
115 120 125

Ile Arg Asp Met Gly Val Gly Gln Ser Ala Val Glu Gln Leu Ala Val
130 135 140

Tyr Cys Val Ser Leu Lys Lys Glu Tyr Glu Asn Leu Lys Glu Ala Arg
145 150 155 160

Lys Ala Thr Gly Glu Leu Ala Asp Arg Leu Lys Lys Asp Leu Val Ser
165 170 175

Ser Arg Ser Lys Leu Lys Thr Leu Asn Thr Glu Leu Asp Gln Ala Lys
180 185 190

Leu Glu Leu Arg Ser Ala Gln Lys Asp Leu Gln Ser Ala Asp Gln Glu
195 200 205

Ile Thr Ser Leu Arg Lys Lys Ser Asp Asp Pro Pro
210 215 220

(2) INFORMATION FOR SEQ ID NO:5:

- Cont
P1*
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Ala Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His Ser Arg Asp
1 5 10 15

Val Ala Ala Met Asp Cys Gly His Thr Phe His Leu Gln Cys Leu Ile
20 25 30

Gln Ser Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln Cys Arg Ile
35 40 45

Gln Val Gly
50

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Ser Leu Cys Thr Ile Cys Ser Asp Phe Phe Asp His Ser Arg Asp
1 5 10 15

Val Ala Ala Ile His Cys Gly His Thr Phe His Leu Gln Cys Leu Ile
20 25 30

Gln Trp Phe Glu Thr Ala Pro Ser Arg Thr Cys Pro Gln Cys Arg Ile
35 40 45

Gln Val Gly
50

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2007 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGCGGTGGA GCGAAATTTG AAGCAAGCGG AGGCAGGGCG CTCTACGAAG CCGGACCTGT 60
AGCAGTTTCT TTGGCTGCCT GGGCCCTTG AGTCCAGCCA TCATGCCTAT CCGTGCTCTG 120
TGCACTATCT GCTCCGACTT CTTCGATCAC TCCCGCGACG TGGCCGCCAT CCACTGCGGC 180
CACACCTTCC ACTTGCAGTG CCTAATTCAAG TCCTTGAGA CAGCACCAAG TCGGACCTGC 240
CCACAGTGCC GAATCCAGGT TGGCAAAAGA ACCATTATCA ATAAGCTCTT CTTTGATCTT 300
GCCCAGGAGG AGGAGAATGT CTTGGATCGA GAATTCTTAA AGAATGAACG GGACAATGTC 360
AGAGCCCAGC TTTCCCAGAA AGACAAGGAG AAACGAGACA GCCAGGTCAT CATCGACACT 420
CTGCGGGATA CGCTGGAAGA ACGCAATGCT ACTGTGGTAT CTCTGCAGCA GGCCCTGGGC 480
AAGGCCGAGA TGCTGTGCTC CACACTGAAA AAGCAGATGA AGTACTTAGA GCAGCAGCAG 540
GATGAGACCA AACAAAGCACA AGAGGAGGCG GCCCGGCTCA GGAGCAAGAT GAAGACCATG 600
GAGCAGATTG AGCTTCTACT CCAGAGCCAG CTCCCTGAGG TGGAGGAGAT GATCCGAGAC 660
ATGGGTGTGG GACAGTCAGC GGTGGAACAG CTGGCTGTGT ACTGTGTGTC TCTCAAGAAA 720
GAGTACGAGA ATCTAAAAGA GGCACGGAAG GCCTCAGGGG AGGTGGCTGA CAAGCTGAGG 780
AAGGATTGT TTTCCCTCCAG AAGCAAGTTG CAGACAGTCT ACTCTGAATT GGATCAGGCC 840
AAGTTAGAAC TGAAGTCAGC CCAGAAGGAC TTACAGAGTG CTGACAAGGA AATCATGAGC 900
CTGAAAAAGA AGCTAACGAT GCTGCAGGAA ACCTTGAACC TGCCACCAAGT GGCCAGTGAG 960
ACTGTCGACC GCCTGGTTTT AGAGAGCCCA GCCCTGTGG AGGTGAATCT GAAGCTCCGC 1020
CGGCCATCCT TCCGTGATGA TATTGATCTC AATGCTACCT TTGATGTGGA TACTCCCCA 1080
GCCCGGCCCT CCAGCTCCCA GCATGGTTAC TACGAAAAAC TTTGCCTAGA GAAGTCACAC 1140
TCCCCAATTC AGGATGTCCC CAAGAAGATA TGCAAAGGCC CCAGGAAGGA GTCCCAGCTC 1200
TCACTGGGTG GCCAGAGCTG TGCAGGAGAG CCAGATGAGG AACTGGTGG TGCCTTCCCT 1260
ATTTTTGTCC GGAATGCCAT CCTAGGCCAG AAACAGCCCA AAAGGCCAG GTCAGAGTCC 1320
TCTTGAGCA AAGATGTGGT AAGGACAGGC TTCGATGGGC TCGGTGGCCG GACAAAATTC 1380
ATCCAGCCTA CTGACACAGT CATGATCCGC CCATTGCCTG TTAAGCCCAA GACCAAGGTT 1440

AAGCAGAGGG TGAGGGTGAA GACCGTGCCT TCTCTTTCC AGGCCAAGCT GGACACCTTC 1500
CTGTGGTCGT GAGAACAGTG AGTCTGACCA ATGGCCAGAC ACATGCCTGC AACTTGAGG 1560
TCAAGGACTG TCCAGGCAGG GTTTGTGGAC AGAGCCCTAC TTTCGGGACC AGCCTGAGGT 1620
GTAAGGGCAG ACAAACAGGT GAGGGTGAGT GTGACACCCA GAGACTGCTC TTCCCTGCCCT 1680
CACCCCTGCC CACTCCTACG ACTGGGAGCT GACATGACCA GCCCACTGAT CCTGTCAGCA 1740
GGTCCTGCTC TGTTGCCAGG CTCTTGTAA TAGCCATGAT CAGATGTGGT CAGACTCTT 1800
CTGGGCCTGG AGACCACGGT CACTTGTGA CTGTCTCTGT GGACCAGAGT GCPTGAGGCA 1860
TCTCAGGCAG CCTCAGCCCCA AGCTTCTACC TGCCCTTGAC TTGCTTCTAG CATAGCCTGG 1920
GCCAAGCAGG GTGGGGAATG GAGGATAGAC ATGGGATGTA TGGAGAGGAT GGAAGATTT 1980
CCCGAAAAAA AAAAAAAA AAAAAAA 2007

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1975 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCACGAGGT GCGGTGGAGC GAAATTGAA GGAACCGGAG CGGTGGCCGG TTCCACCAAA 60
CTGTGTCTGT CTCTGGCAGC TGTTCCCTG GGCTGCTTGA GTGAGCCAT CATGCCTATC 120
CTCTCTCTGT GCACTATCTG CTCCGACTTC TTGATCACT CCCGTGACGT GGCTGCCATC 180
CACTGTGGCC ACACTTTCA TCTGCAATGC CTAATCCAGT GGTTGAGAC AGCACCAAGT 240
CGGACCTGCC CACAGTGTAG AATCCAGGTT GGCAAAAGA CTATTATAAA CAAACTTTTC 300
TTTGACCTCG CCCAGGAAGA GGAGAATGTC TTGGATGCAG AATTCTTAAA GAATGAAC 360
GACAGCGTCA AAGCTCAGCT TTCCCAGAAA GACAGGGAGA AACGGGACAG CCAGGCCATT 420
ATCGACACTC TACGGGACAC CCTGGAAGAA CGCAATGCTA CCGTGGAGTC CCTACAGAAC 480
GCCTTAAACA AGGCAGAGAT GCTGTGTTCC ACCCTGAAAA AACAGATGAA GTTCCTGGAG 540
CAGCGGCAGG ATGAGACCAA ACAAGCTCGG GAGGAGGCC ACCGACTCAA GTGCAAGATG 600
AAAACCATGG AGCAAATTGA GCTCCTACTC CAGAGCCAGC GTTCTGAGGT GGAGGAGATG 660
ATTCGAGACA TGGGTGTGGG ACAGTCAGCG GTGGAGCAGC TGGCTGTGTA CTGCGTGTCC 720
CTCAAGAAAG AGTATGAGAA TCTGAAGGAA GCTCGGAAGG CCACAGGGGA ACTGGCTGAC 780

AGGTTGAAGA AGGATTTGGT GTCCTCTAGG AGCAAGTTGA AGACTCTCAA CACTGAGCTG 840
GATCAGGCCA AGTTAGAACT GAGGTCAGCC CAGAAGGACT TACAAAGTGC TGACCAGGAG 900
ATCACGAGCC TAAGAAAGAA GTCTGATGAT CCTCCAGGG A CCTTGAGCC TGCCTCCCG 960
ACCAATGAGA CGGTCAGCCG CCTGGTTTT GAGAGCCCAG CCCCTGTGGA GATGATGAAC 1020
CCGAGGCTTC ACCAGCCACC CTTCGGTGAT GAGATTGATC TCAATACCAC CTTTGATGTA 1080
AATAACCCCTC CAACCCAGAC CTCTGGCTCC CAGCATTGCC TCCCCAAGAA GCTGTGCCTG 1140
GAGAGGGCAC GCTCTCCCAT GCAGAATGTC CTCAAGAAGG TGCACAAAGT CTCGAAGCCG 1200
GAGTCCCAGC TCTCACTGGG TGGCCAGCGA TGTGTAGGAG AGCTAGATGA GGAACCTGGCT 1260
GGTGCCTTCC CTCTCTTCAT CCGGAATGCT GTCCTGGTC AGAAAACAGCC CAACAGGACC 1320
ACAGCAGAAT CCCGAAGCAG CACAGATGTG GTAAGAATAG GCTTTGATGG GCTTGGAGGA 1380
CGAACAAAAT TCATCCAGCC TAGGGACACA ACCATTATCC GACCAAGTGCC TGTTAAGTCC 1440
AAGGCCAAGA GTAAACAGAA AGTGAGAATA AAGACTGTGA GTTCTGCCTC CCAGCCCAAG 1500
CTGGATAACCT TCTTATGTCA GTGAACGGTG ACCAGAGTGA TGTGCAAT TAGTGGCCA 1560
AGACCTGGCT AACCGGAAGT GTTTTGGAA GATGGCTCCT CTTGGACCAG TCCAAGAGAG 1620
ATGCCAGAA AACACACTTC CTGTGTTCAC TGCGCCCTGC ACCACACTGG GAAGCCACAT 1680
GACCAGTTA CTGTTCCGAT CAGCAGGGCC TACTTCCAGT TGCAAGGTTT TGCTTATAGC 1740
TACAACCAGG TGTGGCTGGA CTCCCTTGT TTTTATAGAA CAGGGTCACA TTGACTCTAA 1800
GTGGATGGGA GTGCTGGAGG ATCCTATGCA GGCTGGAGGA CCCTGCGCTT GAACTCCTGC 1860
CTGCCCTCCAG CTTATTGCTT GAAATTATGG GGTGAGGTGG TGATAGGGAA AGGTTGGGAA 1920
AGTTTTCTGT GTAAAATAAA AAGGGATCTT TTCTTCAAAA AAAAAAAA AAAAAA 1975

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: peptide
 - iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal

(xi) /SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu Gly Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:10:

- Cut B1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln
1 5 10 15

Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu
20 25 30

Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Arg Thr Cys Lys Val Cys Met Asp Arg Glu Val Ser Ile Val Phe
1 5 10 15

Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser Leu
20 25 30

Arg Lys Cys Pro Ile Cys Gly Arg Gly Thr Ile
35 40

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal

*Cont
B)*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Phe Gln Leu Cys Lys Ile Cys Ala Glu Asn Asp Lys Asp Val Lys Ile
1 5 10 15

Glu Pro Cys Gly His Leu Met Cys Thr Ser Cys Leu Thr Ser Trp Gln
20 25 30

Glu Ser Glu Gly Gln Gly Cys Pro Phe Cys Arg Cys Glu Ile Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met Thr
1 5 10 15

Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys Ile Val Thr Ala
20 25 30

Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys Lys Leu Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal

(x) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val Ser
1 5 10 15

Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln Val Gly
20 25 30

Lys Gly Gly Ser Val Cys Ala Val Cys Arg Gln Arg Phe Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(x) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys
1 5 10 15

Leu Arg Ile Leu Pro Cys Ser His Ala Tyr His Cys Lys Cys Val Asp
20 25 30

Pro Trp Leu Thr Lys Thr Lys Thr Cys Pro Val Cys Lys Gln Lys
35 40 45

Val Val
50

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(x) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ala Glu Cys Thr Ile Cys Tyr Glu Asn Pro Ile Asp Ser Val Leu
1 5 10 15

Tyr Met Cys Gly His Met Cys Met Cys Tyr Asp Cys Ala Ile Glu Gln
20 25 30

Trp Arg Gly Val Gly Gly Gln Cys Pro Leu Cys Arg Ala Val Ile
35 40 45

Arg

Crab
B1